BIOTECHNOLOGY
SYSTEMS
~~NCH

CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: __09/097,791A__

#24
Plunkett

Filing Date: __6/16/1998__

Date Processed by STIC: __10/1/2001__

STIC Contact: **Mark Spencer, 703-308-4212**

Nature of Problem:

The CRF (was):

_____ (circle one) Damaged or Unreadable (for Unreadable, see attached)

_____ Blank (no files on CRF) (see attached)

_____ Empty file (filename present, but no bytes in file) (see attached)

_____ Virus-infected. Virus name _____ The STIC will not process the CRF.

_____ Not saved in ASCII text

_____ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should only be the Sequence Listing

_____ Did not contain a Sequence Listing (see attached sample)

_____ Other _____

_____

PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS. SEE BELOW FOR DETAILS:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1631

```
        RAW SEQUENCE LISTING              DATE: 10/01/2001
        PATENT APPLICATION:  US/09/097,791A     TIME: 13:47:11

        Input Set : A:\Sequence 1-25.WorkFile.txt
        Output Set: N:\CRF3\10012001\I097791A.raw
```

W--> 1 Application Project
W--> 2 -------------------
W--> 3 <120> TITLE OF INVENTION: Title : Polymerase Signaling Assay
W--> 0 <110> APPLICANT:
W--> 4 <130> FILE REFERENCE: AppFileReference : 13065
W--> 5 <140> CURRENT APPLICATION NUMBER: CurrentAppNumber : 09/097,791A
C--> 6 <141> CURRENT FILING DATE: 1998-06-16
W--> 8 Sequence
W--> 9 --------

Does Not Comply
Corrected Diskette Needed

sample 1 submitted file

ERRORED SEQUENCES

    10 <213> ORGANISM: OrganismName : Homo sapiens
W--> 0 <160> NUMBER OF SEQ ID NOS:
W--> 11 <210> SEQ ID NO:
W--> 11 <211> LENGTH:
W--> 11 <212> TYPE:
W--> 11 <400> SEQUENCE: PreSequenceString :
    12 gtctctccca ggacaggcac a   21
E--> 13 <212> TYPE: Type : DNA
W--> 14 <211> LENGTH: Length : 21
W--> 15 SequenceName : Sequence 1
W--> 16 SequenceDescription :
W--> 18 Custom Codon
W--> 19 ------------
W--> 20 Sequence Name : Sequence 1
W--> 22 Sequence
W--> 23 --------
    24 <213> ORGANISM: OrganismName : Homo sapiens
W--> 25 <210> SEQ ID NO:
W--> 25 <400> SEQUENCE: PreSequenceString :
    26 gtctctcgca ggacaggcac a   21
E--> 27 <212> TYPE: Type : DNA
W--> 28 <211> LENGTH: Length : 21
W--> 29 SequenceName : Sequence 2
W--> 30 SequenceDescription :
W--> 32 Custom Codon
W--> 33 ------------
W--> 34 Sequence Name : Sequence 2
W--> 36 Sequence
W--> 37 --------
C--> 38 <213> ORGANISM: OrganismName : Artificial/Unknown   *see item 10 on Err Summary Sheet*
W--> 39 <210> SEQ ID NO:
W--> 39 <220> FEATURE:
W--> 39 <223> OTHER INFORMATION:
W--> 39 <400> SEQUENCE: PreSequenceString :

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 0 9/0 9 9, 991 A |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001